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**FIG. 1A-1**

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801 GACTCCTGCC CCAGCTGCTG AAGAGACAAT GACCACCAGC CCGGGGACTC CTGCCCCAGC TGCTGAAGAG ACAATGACCA CCAGCCCCGG GACTCCTGCC  
 CTGAGGACGG GGTGACGAC TTCTCTGTTA CTGGTGGTGG GGGCCCTGAG GACGGGGTGG ACGACTTCTC TGTTACTGGT GGTGGGGCCC CTGAGGACGG  
 204 ThrProAla ProAlaAlaG luGluThrMe tThrThrSer ProGlyThrP roAlaProAl aAlaGluGlu ThrMetThrt hrSerProGl yThrProAla  
 901 TCTTCTCATT ACCTCTCATG CACCATCGTA GGGATCATAG TTCTAATTGT GCTTCTGATT GTGTTTGTTF GAAAGACTTC ACTGTGGAAG AAATTCCTTC  
 AGAAGAGTAA TGGAGAGTAC GTGGTAGCAT CCCTAGTATC AAGATTAAAC CGAAGACTAA CACAAACAAA CTTTCTGAAG TGACACCCTC TTTAAGGAAG  
 237 SerSerHist yrLeuSerCy sThrIleVal GlyIleIlev alLeuIleVa lLeuLeuIle ValPheVal  
 1001 CTTACCTGAA AGGTTCAAGT AGGCGCTGGC TGAGGGGGGG GGGCGCTGGA CACTCTCTGC CCTGCCTCCC TCTGCTGTGT TCCCACAGAC AGAAACGCCT  
 GAATGGACTT TCCAAGTCCA TCCGGGACCG ACTCCGGCCC CCGCGACCT GTGAGAGACG GGACGGAGGG AGACGACACA AGGGTGTCTG TCTTTGCGGA  
 1101 GCCCCTGCCC CAAAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA  
 CCGGACGGG GTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT

FIG.\_1A-2

1 GCTGTGGGAA CCTCTCCAG CGACGAACT CAGCCAAACGA TTCTGATAG ATTTTTGGGA GTTTGACCAG AGATGCAAG GGTGAAGGAG CGCTTCCTAC  
 CGACACCCCTT GGAGAGGTGC GCGTGCTTGA GTCGGTTGCT TAAACACTATC AAAGACTATC TAAACACCT CAAACTGGTC TCTACGTTCC CCACTTCCTC GCGAAGGATG  
 MetGlnGl yValLysGlu ArgPheLeuPro

-40

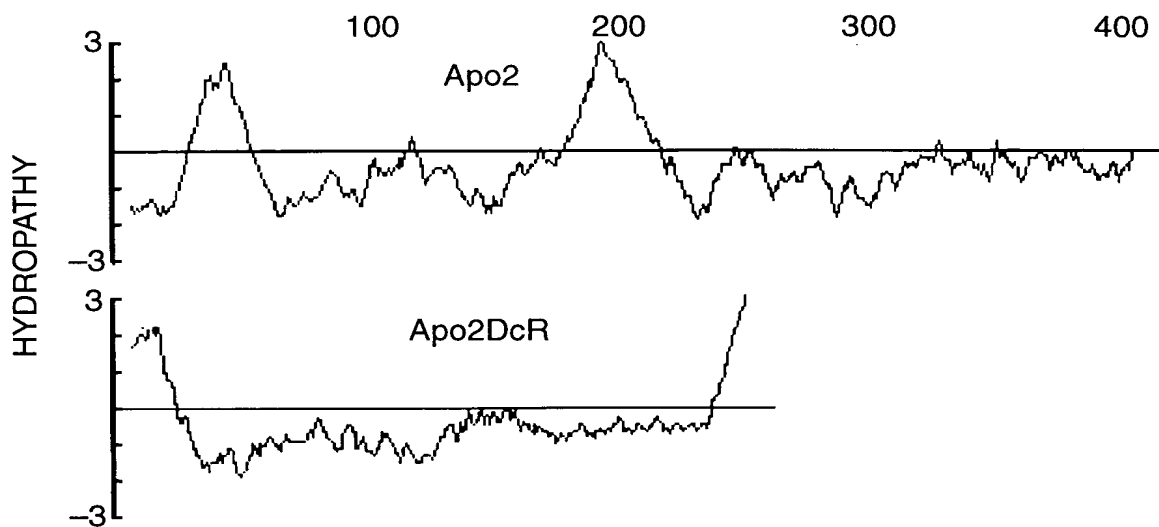
101 CGTTAGGGAA CTCTGGGGAC AGAGCGCCCC GCGCGCCTGA TGGCCGAGGC AGGGTGGAC CCAGGACCCA GGACGGCGTC GGAACCCATA CCATGGCCCCG  
 GCAATCCCTT GAGACCCCTG TCTCGCGGGG CCGGCGGACT ACGGCTCCG TCCCACGCTG GGTCTGGGT CCTGCCGAG CCCTTGGTAT GGTACCGGGC  
 -30 LeuGlyAs nSerGlyAsp ArgAlaProA rgProProAs pglyArgGly ArgValArgP roArgThrGl nAspGlyVal GlyAsnHist hrMetAlaArg  
 201 GATCCCCAAG ACCCTAAAGT TCGTGTGCTG CATCGTCGGC GTCTGTCTGC CAGTCCTAGC CAGCTGCC GGCAGGAGGA AGTCCCCCAG  
 CTAGGGGTC TGGGATTCA AGCAGCAGCA GTAGCAGCG CAGGACGACG GTCAGGATCG AATGAGACGG TGGTACGG CCGTCTCTCT TCAAGGGGTC  
 4 IleProLys ThrLeuLysP heValValVa lIleValAla ValLeuLeuP roValLeuAl aTyrSerAla ThrThrAlaA rgGlnGluGl uValProGln  
 301 CAGACAGTGG CCCCACAGCA ACAGAGGCAC AGCTTCAAG GGGAGGAGTG TCCAGCAGGA TCTCATAGAT CAGAAACATAC TGGAGCCTGT AACCCGTGCA  
 GTCTGTACCC GGGGTGCTGT TGCTCCCGTG TCGAAGTTCC CCGTCTCTAC AGGTGCTCTC AGAGTATCTA GTCTTGTATG ACCTGGGACA TTGGGCACGT  
 37 GlnThrVala laProGlnGl nGlnArgHis SerPheLysG lyGluGluCy sProAlaGly SerHisArgS erGluHisTh rGlyAlaCys AsnProCysThr

FIG.\_1B-1

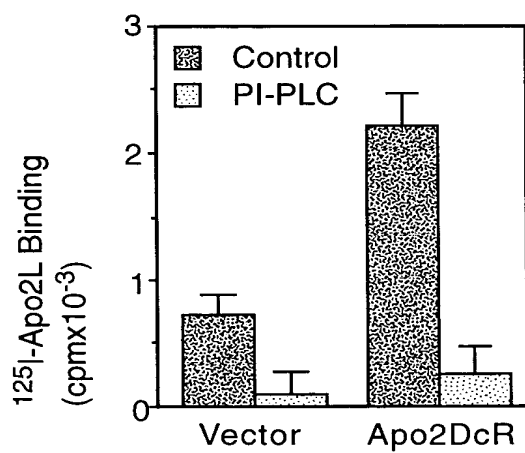


Apo2	1	-----MEQRGQNAFAASGARKRHGPGPREARGARPGLRVPKTLVL
Apo2DcR	1	-----MARIPKTLKEVV
DR4	51	GRGALPTSMGQHGPSARARAGRAPGRPARASPRLRVHKTFKFVVVGVL
Apo2	41	VVAAVLLLVSAESALITQODLAPQORAAPOQKRSSPSEGLCPPGHHISED
Apo2DcR	13	VIVAVLLPVLAYSATTARQEEVPOQTVAPOQQRHSFKGEECPAGSHRSEH
DR4	101	LQVVPSSAATIK-----LHDQSIGTQOWEHSPLGELCPPGSHRSEH
Apo2	91	GRDCISCKYGDYSTHWNDLLECLRCRDSGVEVLSPECTTTRNTVCQCE
Apo2DcR	63	TGACNECTEGVDYTNASNNEPSCFPCTVCKSDQKHKSCTMTTRDTVCQCK
DR4	142	FGACNRCTEGVGYTNASNLLFACLPCTACKSDEEERSPECTTTRNTACQCK
Apo2	141	EGTFREEDSPEMCRKCRGTCPRGMVKVGDCTPWSDIECVHKE-----
Apo2DcR	113	EGTFRNENSPEMCRKCSR-CPSGEVQVSNCTSWDDIQVE-EFGANATVE
DR4	192	FGTFRNNSAEMCRKCSGTCPRGMVKVKDCTPWSDIECVHKE-----
Apo2		-----
Apo2DcR	161	TPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMTTSPGTPAPAAE
DR4		-----
Apo2	183	-----SGIIIGVTVAAVVLIVAVFV---
Apo2DcR	211	ETMTTSPGTPAPAAEETMTTSPGTPASSHYLSCTIVGIIVLIVLLIVFV
DR4	234	-----SGNGHNIWVILVVTLLVVPILLIVAV-LIVC
Apo2	203	CKSLLWKKVLPYLKGICSGGGGDPERVDRSSQRPGAEDNVLNEIVSILQP
DR4	262	CCIGSGCGGDEPKCMDRVCFWRLGLLRGPGAEDNAHNEILSNADSLSTFVS
Apo2	253	TQVPEQEMEVOEPAEFTGVNMLSPGSEHLLPEAEAEISORRRLLVPANE
DR4	312	----EQQMESQEPADLTGVTVQSPGEAQCLLGPAEAEGSORRRLLVPANG
Apo2	303	GDPTETLRQCFDDFADIVPFDSEWELMRKLGIMDNEIKVAKAEAAGH--R
DR4	358	ADPTETLMLFFDKFANIVPFDSDWQLMRQLDITKNEIDVVRAGTAGP--G
Apo3/DR3	338	VMDAVPARRWKEFVRTLGLREAEIEAVEVEI-GRF-R
TNFR1	322	VVENVPPLRWKEFVRRGLSDHEIDRIELON-GRCLR
CD95	220	IAGVHTLSQVKGfVRKNGVNEAKIDEIKNDN-VQDTA
Apo2	351	DILYTMLIKWVNKTGR-DASVHTLLDALETIGERLAKOKIEDHLLSSGKF
DR4	406	DALYAMLMKWVNKTGR-NASHTLLDALERMERHAKKEKIQDLLVDSGKF
Apo3/DR3	374	DQQYEMLKRWRRQQP---AGLGAVYAALERMGLDGCVEDLRS
TNFR1	358	EAQYSMLATWRRRTERRREATLEILGRVLRDMDLLGCLEDIEE
CD95	256	EQKVQILRNWHQLHGKKEAY-DTLIKDLKKANLCTLAEKIQT
Apo2	400	MYLEGNADSALS
DR4	455	IYLEDGTGSAVSL

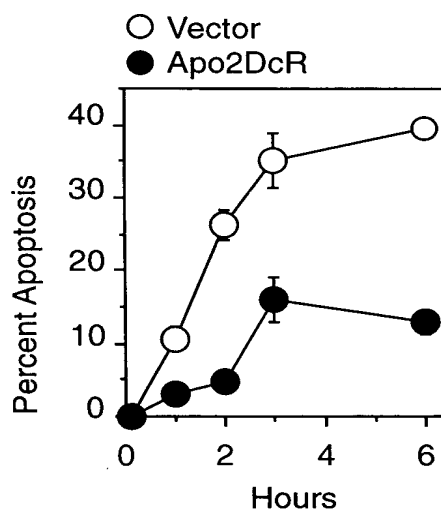
**FIG.\_2**



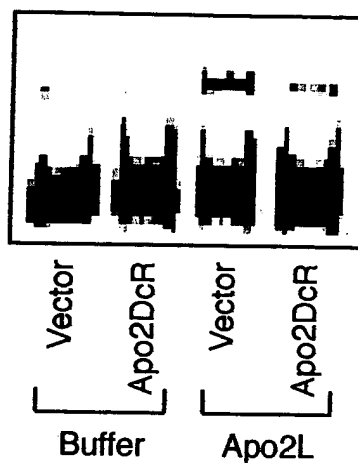
**FIG.\_3**



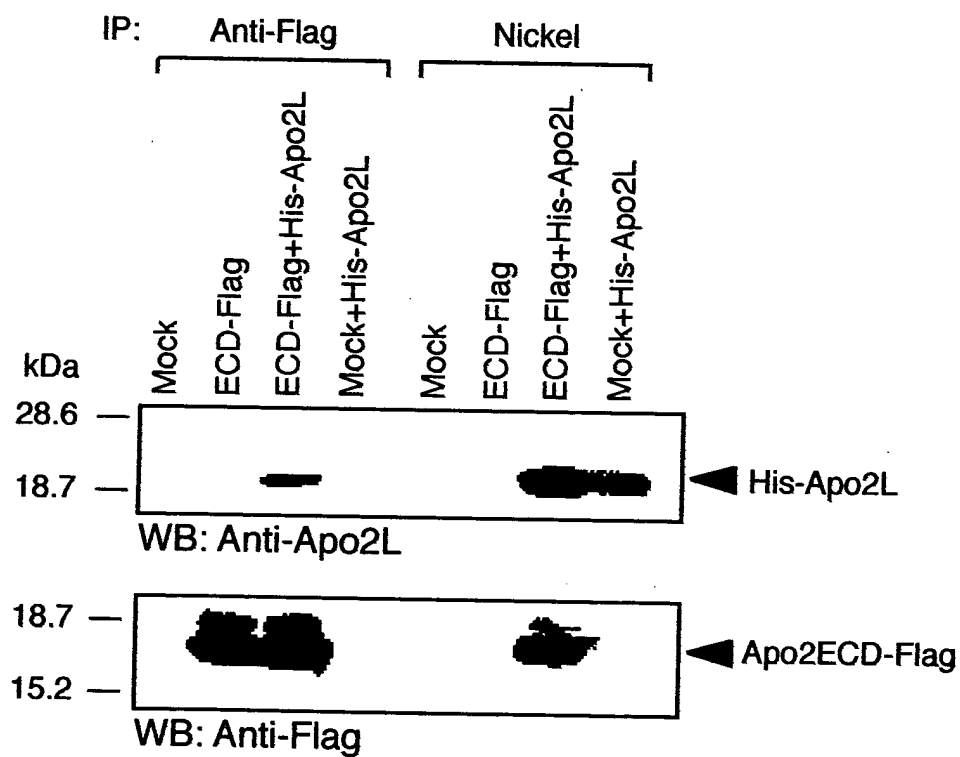
**FIG.\_4**



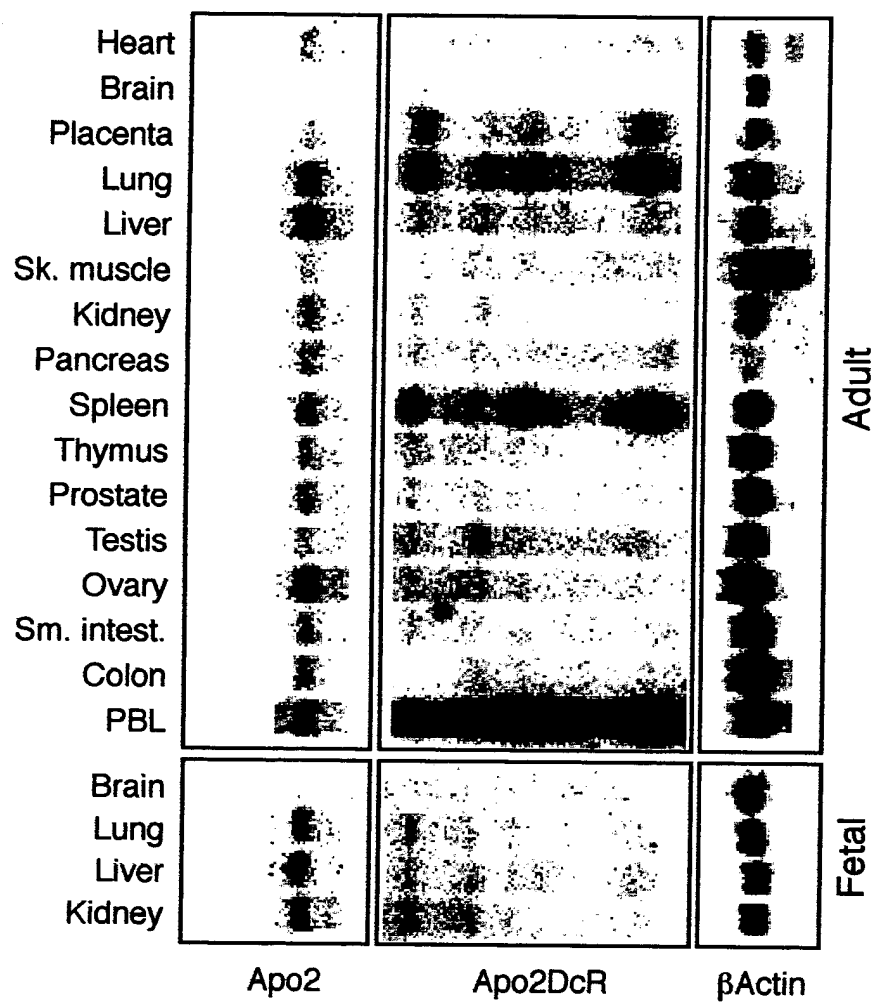
**FIG.\_5**



**FIG.\_6**



**FIG.\_10**



**FIG. 7**

**FIG. 8A-1**



**FIG. 8A-2**

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1101 CCTTTGACTC CTGGGAGCCG CTCATGAGGA AGTTGGGCCT CATGGACAAT GAGATAAAGG TGGCTAAAGC TGAGGCAGCG GGCCACAGGG ACACCTTGTA  
 GGAACACTGAG GACCTCGGC GAGTACTCCT TCAACCCGGA GTACCTGTTA CTCTATTCC ACCGATTTCG ACTCCGTCG CCGGTGTCCT TGTGGAACAT  
 322 PheAspSe rTrpGluPro LeuMetArgL ysLeuGlyLe uMetAspAsn GluileLysV alAlaLysAl aGluAlaAla GlyHisArgA spThrLeuTyr  
 1201 CACGATGCTG ATAAAGTGGG TCAACAAAAC CGGGCGAGAT GCCTCTGTCC ACACCCCTGCT GGATGCCTTG GAGACGCTGG GAGAGAGACT TGCCAAGCAG  
 GTGCTACGAC TATTTCACCC AGTTGTTTGG GCCGCTCTA CCGAGACAGG TGTGGGACGA CCTACGGAAC CTCTGCGACC CTCTCTCTGA ACGGTTCGTC  
 355 ThrMetLeu IleLysTrpV alAsnLysTh rGlyArgAsp AlaSerValH isThrLeule uAspAlaLeu GluThrLeug lyGluArgLe uAlaLysGln  
 1301 AAGATTGAGG ACCACTTGTT GAGCTCTGGA AAGTTCATGT ATCTAGAAGG TAATGCAGAC TCTGCCWTGT CCTAAGTGTG ATTCTCTTCA GGAAGTGAGA  
 TTCTAACTCC TGGTGAACAA CTCGAGACCT TTCAAGTACA TAGATCTTCC ATTACGCTCG AGACGGAACA GGATTACACAC TAAGAGAAAGT CCTTCACACTCT  
 388 LysIleGluA spHisLeuLe uSerSerGly LysPheMetT yrLeuGluGl yAsnAlaAsp SerAlaXq4S erOC\*  
 1401 CCTTCCCTGG TTACCTTTT TTCTGGAAAA AGCCCAACTG GACTCCAGTC AGTAGGAAG TGCCACAATT GTCACATGAC CGGTACTGGA AGAAACTCTC  
 GGAAGGGACC AAATGGAAAA AAGACCTTTT TCGGCTGAC CTGAGGTCAG TCATCCCTTC ACGGTCTTAA CAGTGTACTG GCCATGACCT TCTTTGAGAG  
 1501 CCATCCAACA TCACCCAGTG GATGGAACAT CCTGTAACCT TTCACTGCAC TTGGCATTAT TTTTATAAGC TGAATGTGAT AATAAGGACA CTATGGAAT  
 GGTAGGTTGT AGTGGGTCAC CTACCTTGTA GGACATTGAA AAGTGACGTG AACCGTAATA AAAATATTGG ACTTACACTA TTATTCCCTGT GATACCTTTA  
 1601 GTCTGGATCA TTCCGTTTGT GCGTACTTTG AGATTGTTT TGGGATGTC TTTGTTTTCAC AGCACCTTTT TATCCTAATG TAAATGCCTT ATTTATTTAT  
 CAGACCTAGT AAGGCAACA CGCATGAAC TCATAACCAA ACCCTACAGT ACAAAGCTG TCGTGAAAAA ATAGGATTAC ATTTACGAAA TAAATAAATA  
 1701 TTGGGGTACA TTGTAAGATC CATCTACAA AAAAAAAA GGGGGCCGCG ACTCTAGAGT CGACCTGCAG AAGCTTGCC GCCATGGCC  
 AACCCGATGT AACATTCTAG GTAGATGTTT TTTTTTTTTT TTTTTTTTTT CCGCCGGCGC TGAGATCTCA GCTGGACGTC TTCGAACCGG CCGTACCGG

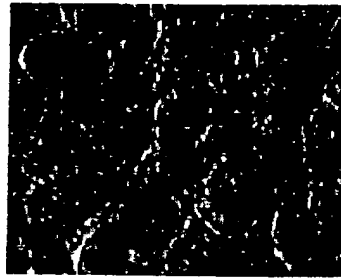
FIG.-8B

1 MEORGQNA PAA SGARKRHGPGPREARGARPLRVKTLVLVVAAVLLLVSAESALITQQD  
 61 LAPQORAA PQKRSSPSEGLCPPGHHISEDGRDCISCKYGQDYSTHWNDDLFLCLRCTRCD  
 121 SGEVELSPCTTTRNTVCQEEGTFREEDSPEMCRKQRTGCPRGMVKVGDCPTWSDIECVH  
 181 KESGIIIGVTVA AVLIVAVFVCKSLMKKVLPLYKIGICSGGGDPERVDRSSQRPGEAD  
 241 NVLNEIVSILQPTQVPEQEMEVQEPAEPTGVNMLSPGESEHLLLEPAEAERSQRRLLVPA  
 301 NEGDPTETLRQCFFDDFADLVFPFDSWEPLMRKLGMDNEIKVAKAEAAAGHRDTLYTMLIKW  
 361 VNKTGRDASVHTLLDLETLGERLAKQKIEDHLLSSGKFMYLEGNADSALS

FIG.-9

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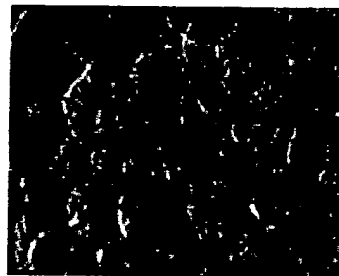
Vector



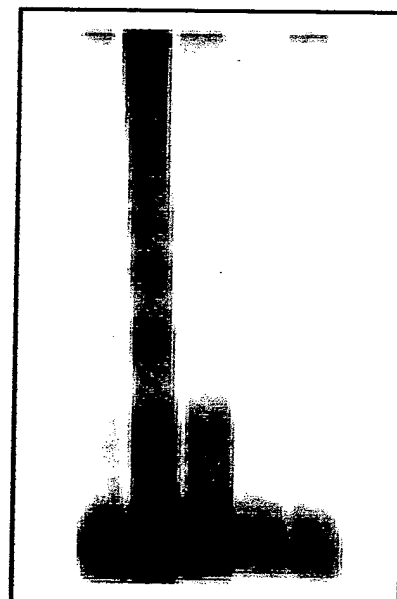
Apo2



Apo2+CrmA



**FIG.\_11A**



Vector

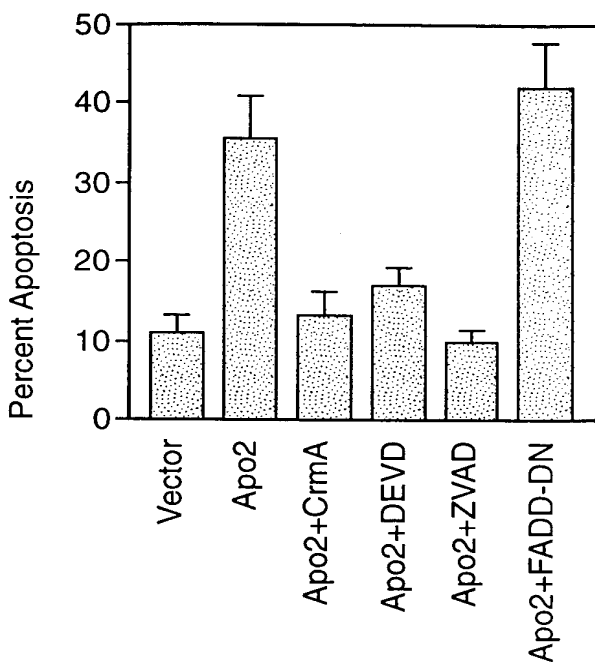
Apo2

Apo2+CrmA

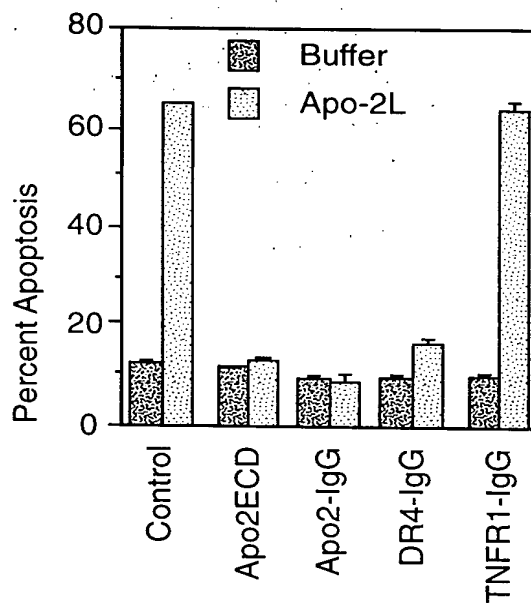
Apo2+DEVD

Apo2+ZVAD

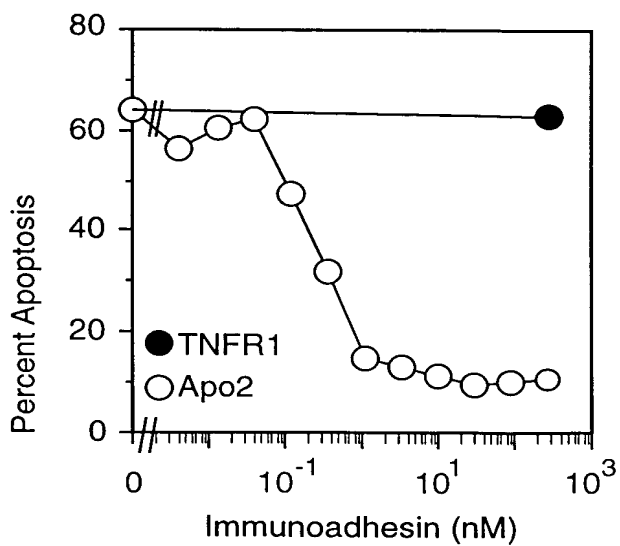
**FIG.\_11B**



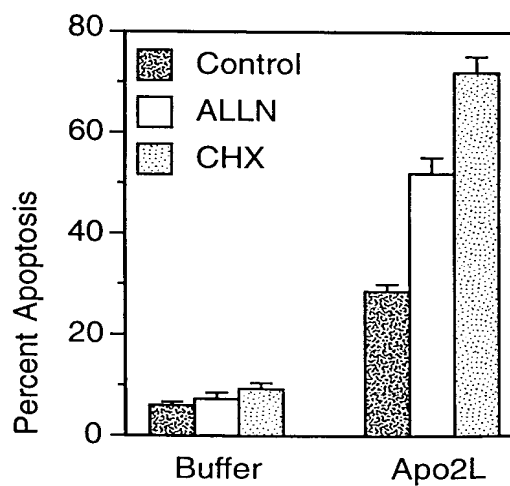
**FIG.\_11C**



**FIG.\_11D**



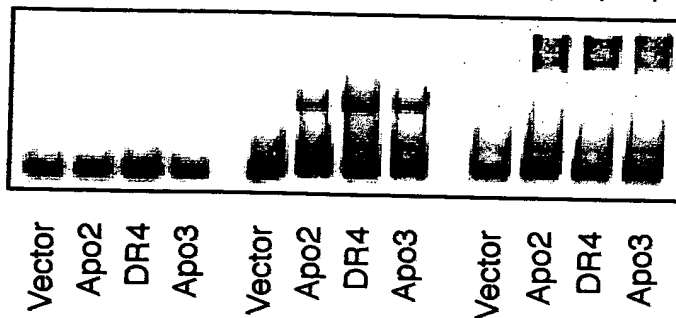
**FIG.\_11E**



**FIG.\_12C**

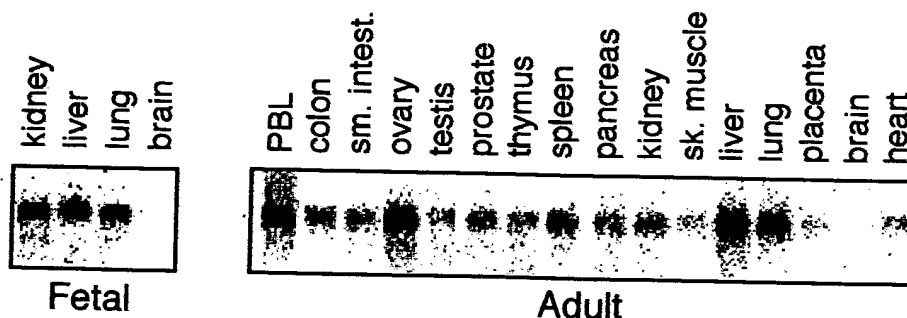
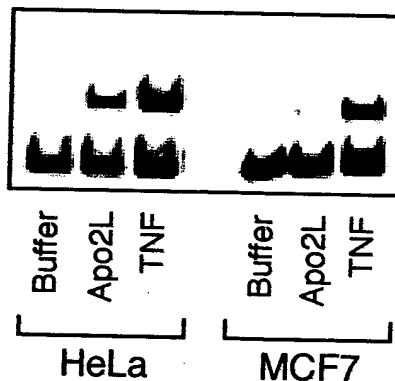
Unlabelled probe	+	+	+	+	-	-	-	-	-	-	-	-
Labelled probe	+	+	+	+	+	+	+	+	+	+	+	+
Anti-p65	-	-	-	-	-	-	-	-	+	+	+	+

**FIG. 12A**



Unlabelled probe	-	-	-	-	-	-
Labelled probe	+	+	+	+	+	+
Anti-p65	-	-	-	-	-	-

**FIG. 12B**



**FIG. 13**